Blast 2 S qu nc s results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix [BLOSUM62 ◆] gap open:[11] gap extension: [1]
x_dropoff: [50] expect:[10.00]wordsize: [3] Filter   [Align]

Sequence 1 gi 3702836   hASIC3 [Homo sapiens]   Length 531
Sequence 2 gi 13592019 P2X3 [Rattus norvegicus] Length 397
N significant similarity was found

Align two sequences

Tue Apr 15 17:04:02 BST 2003

```
/usr/tmp/seq1.214485.sca :   397 aa
>gi|13592019|ref|NP_112337.1| P2X3   [Rattus norve    397 aa vs.
>gi|3702836|gb|AAC62935.1| hASIC3 [Homo sapiens],     531 aa
scoring matrix: , gap penalties: -12/-2
15.7% identity;  Global alignment score: -167
```

```
              10            20            30          40
/usr/t MNCIS----------DFFTYETTKSV-----VVKSWTI----GIINRAVQLLIISYFVGW
       :.  :           :.  .. .. :.       :     ..      :.    :: :  ...
gi|370 MKPTSGPEEARRQPSDIRVFASNCSMHGLGHVFGPGSLSLRRGMWAAAVVLSVATFLYQV
               10            20            30          40          50          60

             50            60            70
/usr/t V-------FLHEKAYQVRDT---AIESSVVTKVKGFGR---------YANRVM---DVS
       .         : :.  :  . :..     ..  .. ... . :        .:.  ..    :  .
gi|370 AERVRYYREFHHQTALDERESHRLVFPAVTLCNINPLRRSRLTPNDLHWAGSALLGLDPA
               70            80            90          100         110         120

80            90           100          110   120         130
/usr/t DYVT-------PPQGTSVFVIITKIIVTENQMQGFCPENEEKYRCVSDSQ-CGPERFPGG
       . . . .       ::      .  :.       .  ...    ..      :     .:  :::::  :
gi|370 EHAAFLRALGRPPAPPG-FMPSPTFDMAQLYARAGHSLDDMLLDCRFRGQPCGPENFTTI
               130           140           150         160         170

            140                        150
/usr/t GILTGRCVNYSS------VLRTC-----------EIQG------W-----CPTEVD---
       :.:  ...:            .:  :             ..:        :          :  ::
gi|370 FTRMGKCYTFNSGADGAELLTTTRGGMGNGLDIMLDVQQEEYLPVWRDNEETPFEVGIRV
       180           190           200         210         220         230

           160           170           180         190         200
/usr/t ---TVEMPIMME------AENFTIFI---KNSIRF---PLFNFEKGNLLPNLTDKDIKRC
         . :  : ...     . .. :.    .... :     :     ...:  ::      .
gi|370 QIHSQEEPPIIDQLGLGVSPGYQTFVSCQQQQLSFLPPPWGDCSSASLNPNY-EPEPSDP
       240           250           260         270         280         290

          210           220           230         240         250         260
/usr/t RFHPEKAPFCPILRVGDVVKFAGQDFAKLARTGGVLGIKIGW---VCDLDKAWDQCIPKY
       :    .:    :    .,: .        .:: .        ::.   .  . .:
gi|370 LGSPSPSPSPPYTLMG--CRLACET-RYVARKCGCRMVYMPGDVPVCS-PQQYKNC----
       300           310           320         330         340         350

          270           280           290                   300
/usr/t SFTRLDGVSEKSSVS---PGYNFRFAKYYKM---ENGSEYRTLLK-------------A
       .   .:.. .:.: .      :   . :.::   .:     . ,  : : .           :
gi|370 AHPAIDAILRKDSCACPNPCASTRYAKELSMVRIPSRAAARFLARKLNRSEAYIAENVLA
               360           370           380         390         400         410
```

```
                  310           320       330           340
/usr/t  FGIRFDVLVYGNAGK------FNIIPTIISSVAAFTSVGVGTVL------CDII---LLN
          . : :..: : .. .      ...  : .... : .... :.:    :...   .:.
gi|370  LDIFFEALNYETVEQKKAYEMSELLGDIGGQMGLFIGASLLTILEILDYLCEVFRDKVLG
              420       430       440       450       460       470


                  350       360       370           380       390
/usr/t  FLKGADHYKARKFEEVTETTLKGTASTN-------PVFASDQATVEKQSTDSG--AYSIG
          .. . .: . ..  .. . : :. :.     :   .   .: :  . :   : .
gi|370  YFWNRQHSQRHSSTNLLQEGL-GSHRTQVPHLSLGPRPPTPPCAVTKTLSASHRTCYLVT
                480 .      490       500       510       520


/usr/t  H-
          .
gi|370  QL
            530
```

Elapsed time: 0:00:00

NCBI

Blast 2 Sequences results

| PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure |

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix [BLOSUM62 ÷] gap open:[11] gap extension: [1]
x_dropoff: [50] expect:[10.00]wordsize: [3] Filter   [Align]

Sequence 1 gi 3702836 proton-gated cation channel subunit [Homo sapiens]   Length 531

Sequence 2 gi 12643353 P2X purinoceptor 2 (ATP receptor) (P2X2) (Purinergic receptor) Length 471

No significant similarity was found

Sequence Alignment Output

Align two sequences

Tue Apr 15 18:49:23 BST 2003

```
/usr/tmp/seq1.215975.sca :  472 aa
>gi|1352688|sp|P49653|P2X2_RAT P2X purinoceptor 2    472 aa vs.
>gi|3702836|gb|AAC62935.1| hASIC3 [Homo sapiens],    531 aa
scoring matrix: , gap penalties: -12/-2
17.1% identity;  Global alignment score: -108


                    10         20        30        40
/usr/t M---------------VRRLARGC-WSAFWDYETPKVIVVRNRRLGFVHRMVQLLILLYF
        :           .: .: .:     ..     :  . .: :  .   .... .::
gi|370 MKPTSGPEEARRQPSDIRVFASNCSMHGLGHVFGPGSLSLR-RGMWAAAVVLSVATFLYQ
            10        20        30        40        50


              50         60         70        80
/usr/t V------WYVFIVQKSYQDSETG----PESSI--ITKVKGITMSEDKV-WDVEEYV--KP
        :       . :  :. .. :.     :  ..   .   .. ..:    .   .  :
gi|370 VAERVRYYREFHHQTALDERESHRLVFPAVTLCNINPLRRSRLTPNDLHWAGSALLGLDP
       60        70        80        90       100       110


       90        100       110       120       130       140
/usr/t PEGGSVVSIITRIEVTPSQTLGTCPESMRVHSSTCHSDDDCIAGQLDMQGNGIRTGHCVP
        : ..   .: .  :.      .  .... . :: ::. .  :: .  .: :  : :
gi|370 AEHAAFLRALGRPPAPPGFMPSPTFDMAQLYARAGHSLDDML---LDCR---FRGQPCGP
       120       130       140       150       160       170


       150       160       170       180       190       200
/usr/t YYHGDSKTCEVSAWCPVEDGTSDNHFL-----GKMAPNFTIL--IKNSIHYPKFKFSKGN
          .        . :  .. .:.  :      : :. .. !.   ... . :.  :
gi|370 ENF--TTIFTRMGKCYTFNSGADGAELLTTTRGGMGNGLDIMLDVQQEEYLPVWR---DN
          180       190       200       210       220


       210       220       230       240       250       260
/usr/t IASQKSDYLKHCTFDQDSDPYCPIFRLGFIVEKAGENFTELAHKGGVIGVIINWNCDLDL
         ..            .:.  :    :  .:::.  :  . ..:.   ..   .  :.  :
gi|370 EETPFEVGIRVQIHSQEEPPI--IDQLGLGVSPGYQTFVSCQQQQLSF-LPPPWG---DC
       230       240       250       260       270       280


       270       280       290       300       310
/usr/t SESECNPKYSFRRLDPKYDPASSGYNFRFAKYYKING---TTTTRTLIKAYGIRIDVIVH
       :  .  ::.:   .   :: .:!. :      .  : .:     ::  .  : :. :  .
gi|370 SSASLNPNYEPEPSDPLGSPSPSP-----SPPYTLMGCRLACETRYVARKCGCRM-VYMP
         290       300       310       320       330


       320       330       340       350       360       370
/usr/t GQAGKFSLIPTIINLATALTSI-GVGSFLCDWILLTFMNKNKLYSHKKFDKVRTPKHPSS
       :..           :. .:     :   . .      :. :,.. :: :... ..
gi|370 GDVPVCSPQQYKNCAHPAIDAILRKDSCACPNPCASTR-----YA-KELSMVRIPSRAAA
       340       350       360       370       380       390
```

Sequence Alignment Output

```
              380                 390        400        410                 420
/usr/t RW--------PVTLA---LVLGQIPPPPSHYSQDQPPSPPSGE-----GPTLGE--GAEL
       :.          . .:   :..:  .    .. . .:   .    .:    :  .:   :: :
gi|370 RFLARKLNRSEAYIAENVLALDIFFEALNYETVEQKKAYEMSELLGDIGGQMGLFIGASL
              400        410        420        430        440        450


              430                          440                   450
/usr/t PLAVQS-PRPCSI-------------------SALTEQVVDTLGQH--------MGQRPPVP
         ..        :  .              . :. . . ::.:        .: :::.:
gi|370 LTILEILDYLCEVFRDKVLGYFWNRQHSQRHSSTNLLQEGLGSHRTQVPHLSLGPRPPTP
              460        470        480        490        500        510


              460        470
/usr/t EPSQQDSTSTDPKG---LAQL
        .     . :.. .    ..::
gi|370 PCAVTKTLSASHRTCYLVTQL
              520        530
```

Elapsed time: 0:00:00